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cat att tta tct gtt ctc ccc caa atc aaa agc act agc ttt ttt g His Ile Leu Ser Val Leu Pro Gln Ile Lys Ser Thr Ser Phe Phe A 100 105 110	
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cca cca gca cca cct cca cca aac ata ctg cca aca cca tca ctg g Pro Pro Ala Pro Pro Pro Pro Asn Ile Leu Pro Thr Pro Ser Leu G 165 170 175	· . ·
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Arg Cys Arg Asp His Cys Asn Val Asp Glu Lys Glu Ile Gln Lys Cys 35 40 45

Lys Met Lys Lys Cys Cys Val Gly Pro Lys Val Val Lys Leu Ile Lys 50 55 60

Asn Tyr Leu Gln Tyr Gly Thr Pro Asn Val Leu Asn Glu Asp Val Gln 65 70 75 80

Glu Met Leu Lys Pro Ala Lys Asn Ser Ser Ala Val Ile Gln Arg Lys 85 90 95

His Ile Leu Ser Val Leu Pro Gln Ile Lys Ser Thr Ser Phe Phe Ala 100 105 110

Asn Thr Asn Phe Val Ile Ile Pro Asn Ala Thr Pro Met Asn Ser Ala 115 120 125

Thr Ile Ser Thr Met Thr Pro Gly Gln Ile Thr Tyr Thr Ala Thr Ser 130 135 140

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aat ac			_										384
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Arg Cys Arg Asp His Cys Asn Val Asp Glu Lys Glu Ile Gln Lys Cys 35 40 45

Lys Met Lys Lys Cys Cys Val Gly Pro Lys Val Val Lys Leu Ile Lys 50 55 60

Asn Tyr Leu Gln Tyr Gly Thr Pro Asn Val Leu Asn Glu Asp Val Gln 65 70 75 80

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His Ile Leu Ser Val Leu Pro Gln Ile Lys Ser Thr Ser Phe Phe Ala 100 105 110

Asn Thr Asn Phe Val Ile Ile Pro Asn Ala Thr Pro Met Asn Ser Ala 115 120 125

Thr Ile Ser Thr Met Thr Pro Gly Gln Ile Thr Tyr Thr Ala Thr Ser 130 135 140

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96

gtg atc cca gcc tat agt ggt gaa aaa aaa tgc tgg aac aga tca ggg

Val	Ile	Pro	Ala 20	Tyr	Ser	Gly	Glu	Lys 25	Lys	Cys	Trp	Asn	Arg 30	Ser	Gly	
		agg Arg 35														144
		ctt Leu														192
_		gcg Ala														240
		gat Asp														288
		aag Lys														336
		tct Ser 115				_					tga					372
<210 <211		42 123								•						
		PRT Homo 42	sapi	iens									•			
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Glu Thr Ser Leu Pro Asn Val His His Ser Ser 115 120	
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cac tgc agg aaa caa tgc aaa gat gga gaa gca gtg His Cys Arg Lys Gln Cys Lys Asp Gly Glu Ala Val 35 40	
aaa aat ctt cga gct tgc tgc att cca tcc aat gaa Lys Asn Leu Arg Ala Cys Cys Ile Pro Ser Asn Glu 50 55 60	
gtt cct gcg aca tct ccc aca ccc ttg agt gac tca Val Pro Ala Thr Ser Pro Thr Pro Leu Ser Asp Ser 65 70 75	
att gat gat att tta aca gta agg ttc acg aca gac Ile Asp Asp Ile Leu Thr Val Arg Phe Thr Thr Asp 85 90	
agc agc aag aaa gat atg gtt gaa gag tct gag gcg Ser Ser Lys Lys Asp Met Val Glu Glu Ser Glu Ala 100 105	
gag acc tct ctt cca aat gtt cac cat agc tca tga Glu Thr Ser Leu Pro Asn Val His His Ser Ser 115 120	372
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Val Ile Pro Ala Tyr Ser Gly Glu Lys Lys Cys Trp 20 25	Asn Arg Ser Gly 30

23

His Cys Arg Lys Gln Cys Lys Asp Gly Glu Ala Val Lys Asp Thr Cys 45 35 40 Lys Asn Leu Arg Ala Cys Cys Ile Pro Ser Asn Glu Asp His Arg Arg 60 50 55 Val Pro Ala Thr Ser Pro Thr Pro Leu Ser Asp Ser Thr Pro Gly Ile 75 80 65 70 Ile Asp Asp Ile Leu Thr Val Arg Phe Thr Thr Asp Tyr Phe Glu Val 85 90 95 Ser Ser Lys Lys Asp Met Val Glu Glu Ser Glu Ala Gly Arg Gly Thr 100 105 110 Glu Thr Ser Leu Pro Asn Val His His Ser Ser 120 115 <210> 45 <211> 20 <212> DNA <213> Artificial Sequence <220> <223> PCR primer <400> 45 20 aggttgagta tttgccagac <210> 46 <211> 19 <212> DNA <213> Artificial Sequence <220> <223> PCR primer <400> 46 19 aggacagggg tgagtgata <210> 47 <211> 246 <212> DNA <213> Homo sapiens <220> <221> CDS <222> (1)..(246) <223> Coding sequence for the variant human DEFB126 gene <400> 47 48 atg aag tcc cta ctg ttc acc ctt gca gtt ttt atg ctc ctg gcc caa Met Lys Ser Leu Leu Phe Thr Leu Ala Val Phe Met Leu Leu Ala Gln 15 5 10 1 96 ttg gtc tca ggt aat tgg tat gtg aaa aag tgt cta aac gac gtt gga Leu Val Ser Gly Asn Trp Tyr Val Lys Lys Cys Leu Asn Asp Val Gly

25

30

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		aag Lys 35														,	144
	_	atg Met		-													192
		atc Ile	<del>-</del>					_								:	240
cag Gln	taa															•	246
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Leu	Val	Ser	Gly 20	Asn	Trp	Tyr	Val	Lys 25	Lys	Cys	Leu	Asn	Asp 30	Val	Gly		
Ile	Cys	Lys 35	Lys	Lys	Cys	Lys	Pro 40	Glu	Glu	Met	His	Val 45	Lys	Asn	Gly		
Trp	Ala 50	Met	Cys	Gly	Lys	Gly 55	Thr	Ala	Val	Phe	Gln 60	Leu	Thr	Asp	Val		
Leu 65	Ile	Ile	Leu	Phe	Ser 70	Val	Ser	Arg	Gln	Arg 75	Leu	Gln	Glu	Phe	Gln 80		
Gln																	
	>      >      >    > (	49 336 DNA Homo CDS (1)	. (336	5)		√ <b>ታ</b> ትጌ	,	ım~~	רום ביד	21 <i>06</i>	~~~						
<400	> 4	Codir 49		_													4.0
-		tcc Ser								•							48

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Leu Val Ser	Gly Asn 20	Trp T	Tyr Val	Lys 25	Lys	Cys	Leu	Asn	Asp 30	Val	Gly	
att tgc aag Ile Cys Lys 35	aag aag Lys Lys	tgc a Cys I	aaa cct Lys Pro 40	gaa Glu	gag Glu	atg Met	cat His	gta Val 45	aag Lys	aat Asn	ggt Gly	144
tgg gca atg Trp Ala Met 50		Lys (										192
cgt gct aat Arg Ala Asn 65												240
tca aca gta Ser Thr Val	<del>-</del>											288
gct tcg atg Ala Ser Met	_		_			_					_	336
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1	5 Gly Asn 20	Trp 1	Tyr Val	Lys 25	10 Lys	Cys	Leu	Asn	Asp 30	15 Val	Gly	
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Leu Val Ser  Cys Lys 35  Trp Ala Met	Gly Asn 20 Lys Lys Cys Gly	Trp T	Tyr Val Lys Pro 40 Gln Arc	Lys 25 Glu Asp	Lys Glu Cys	Cys Met	Leu His Val 60	Asn Val 45	Asp 30 Lys	Val Asn Asp	Gly Gly Arg	
Leu Val Ser  Cys Lys 35  Trp Ala Met 50  Arg Ala Asn	Gly Asn 20 Lys Cys Gly Tyr Pro	Trp T	Tyr Val Lys Pro 40 Gln Arc 55	Lys 25 Glu Asp	Lys Glu Cys	Cys Met Cys Thr 75	Leu His Val 60	Asn Val 45 Pro	Asp 30 Lys Ala	Val Asn Asp	Gly Gly Arg Ile 80	
Leu Val Ser  Cys Lys 35  Trp Ala Met 50  Arg Ala Asn 65	Gly Asn 20 Lys Cys Gly Tyr Pro	Trp T	Tyr Val Lys Pro 40 Gln Arg 55 Phe Cys	Lys 25 Glu Asp Val	Lys Glu Cys Gln Thr 90	Cys Met Cys Thr 75	Leu His Val 60 Lys	Asn Val 45 Pro Thr	Asp 30 Lys Ala Thr	Val Asn Asp Thr 95	Gly Gly Arg Ile 80	

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1 10 15	
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ttg gtc tca ggt aat tgg tat gtg aaa aag tgt cta aac gac gtt gga Leu Val Ser Gly Asn Trp Tyr Val Lys Lys Cys Leu Asn Asp Val Gly 20 25 30	96
Leu Val Ser Gly Asn Trp Tyr Val Lys Lys Cys Leu Asn Asp Val Gly 20 25 30	
Leu Val Ser Gly Asn Trp Tyr Val Lys Lys Cys Leu Asn Asp Val Gly 25 30 att tgc aag aag tgc aaa cct gaa gag atg cat gta aag aat ggt	96 144
Leu Val Ser Gly Asn Trp Tyr Val Lys Lys Cys Leu Asn Asp Val Gly 20 25 30	
Leu Val Ser Gly Asn Trp Tyr Val Lys Lys Cys Leu Asn Asp Val Gly 20 25 30  att tgc aag aag tgc aaa cct gaa gag atg cat gta aag aat ggt Ile Cys Lys Lys Lys Cys Lys Pro Glu Glu Met His Val Lys Asn Gly 35 40 45	
Leu Val Ser Gly Asn Trp Tyr Val Lys Lys Cys Leu Asn Asp Val Gly 25 at tgc aag aag aag aat ggt Ile Cys Lys Lys Lys Cys Lys Pro Glu Glu Met His Val Lys Asn Gly 45 tgg gca atg tgc ggc aaa caa agg gac tgc tgt gtt cca gct gac aga Trp Ala Met Cys Gly Lys Gln Arg Asp Cys Cys Val Pro Ala Asp Arg	144
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Leu Val Ser Gly Asn Trp Tyr Val Lys Lys Cys Leu Asn Asp Val Gly 25 aaa cct gaa gag atg cat gta aag aat ggt Ile Cys Lys Lys Lys Lys Cys Lys Pro Glu Glu Met His Val Lys Asn Gly 40 45 tgg gca atg tgc ggc aaa caa agg gac tgc tgt gtt cca gct gac aga Trp Ala Met Cys Gly Lys Gln Arg Asp Cys Cys Val Pro Ala Asp Arg 50 cgt gat tat cct gtt ttc tgt gtc cag aca aag act aca aga att Arg Ala Asn Tyr Pro Val Phe Cys Val Gln Thr Lys Thr Thr Arg Ile	144 192
Leu Val Ser Gly Asn Trp Tyr Val Lys Lys Cys Leu Asn Asp Val Gly 25 aaa cct gaa gag atg cat gta aag aat ggt Ile Cys Lys Lys Lys Cys Lys Pro Glu Glu Met His Val Lys Asn Gly 40 45  tgg gca atg tgc ggc aaa caa agg gac tgc tgt gtt cca gct gac aga Trp Ala Met Cys Gly Lys Gln Arg Asp Cys Cys Val Pro Ala Asp Arg 50 55 C 60  cgt gct aat tat cct gtt ttc tgt gtc cag aca aag act aca aga att Arg Ala Asn Tyr Pro Val Phe Cys Val Gln Thr Lys Thr Thr Arg Ile 65 70 80	144 192 240
Leu Val Ser Gly Asn Trp Tyr Val Lys Lys Cys Leu Asn Asp Val Gly 20 25	144 192
Leu Val Ser Gly Asn Trp Tyr Val Lys Lys Cys Leu Asn Asp Val Gly 25 aaa cct gaa gag atg cat gta aag aat ggt Ile Cys Lys Lys Lys Cys Lys Pro Glu Glu Met His Val Lys Asn Gly 40 45  tgg gca atg tgc ggc aaa caa agg gac tgc tgt gtt cca gct gac aga Trp Ala Met Cys Gly Lys Gln Arg Asp Cys Cys Val Pro Ala Asp Arg 50 55 C 60  cgt gct aat tat cct gtt ttc tgt gtc cag aca aag act aca aga att Arg Ala Asn Tyr Pro Val Phe Cys Val Gln Thr Lys Thr Thr Arg Ile 65 70 80	144 192 240
Leu Val Ser Gly Asn Trp Tyr Val Lys Lys Cys Leu Asn Asp Val Gly 25    att tgc aag aag aag tgc aaa cct gaa gag atg cat gta aag aat ggt Ile Cys Lys Lys Lys Lys Cys Lys Pro Glu Glu Met His Val Lys Asn Gly 40    tgg gca atg tgc ggc aaa caa agg gac tgc tgt gtt cca gct gac aga Trp Ala Met Cys Gly Lys Gln Arg Asp Cys Cys Val Pro Ala Asp Arg 50    cgt gct aat tat cct gtt ttc tgt gtc cag aca aca agg act aca aga att Arg Ala Asn Tyr Pro Val Phe Cys Val Gln Thr Lys Thr Thr Arg Ile 65    tca aca gta aca gca aca aca gca aca aca aca act ttg atg atg act act Ser Thr Val Thr Ala Thr Thr Ala Thr Thr Thr Leu Met Met Thr Thr	144 192 240

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27

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50

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<210> 55

<211> 111

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Trp Ala Met Cys Gly Lys Gln Arg Asp Cys Cys Val Pro Ala Asp Arg 50 55

Arg Ala Asn Tyr Pro Val Phe Cys Val Gln Thr Lys Thr Thr Arg Ile 70 75 80

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